



#4A
5-12-02

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Keegan, Kathleen S.
- (ii) TITLE OF INVENTION: Novel CREBa Isoform
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Marshall, Gerstein & Borun
 - (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/884,566
 - (B) FILING DATE: 2001-06-19
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Williams Jr., Joseph A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/37497
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312-474-6300
 - (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 304..1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTTTG CTTCTTTTG GATGCACAGC	60
CCGATTTAAC CCCTGCACCT TCCGCCCGAT CCCAGCAGGC TTGTCTCCC CGGGGAGTCA	120
CAGATTTC CG AGGACAAGGG TCGCGTAGCC TTCGGCAGGG CTCTCCCGAG TTCCTGCTCC	180
AGTGCATAAG TTCCACGCGC GCACACGCCA AGTACACGGG GAGAAGCGTC TCACCGGCC	240
GCGGCGGCTC TCGCGGTCC CCTCTGCCT CAGCATCCTC GGGCCTGCGC GCGCCCCACC	300

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GCC Met 1	ATG Glu 1	GAG Val 1	GTG Val 1	CTG Leu 1	GAG Glu 5	AGC Ser 5	GGG Gly 5	GAG Glu 5	CAG Gln 5	AGC Ser 10	GTC Val 10	CTG Leu 10	CAG Gln 10	TGG Trp 15	GAC Asp 15	348
CGC Arg	AAG Lys	CTG Leu	AGC Ser	GAG Glu 20	CTG Leu 20	TCA Ser	GAG Glu	CCC Pro	GGA Gly 25	GAG Glu	ACT Thr	GAG Glu	GCC Ala	CTC Leu 30	ATG Met	396
TAC Tyr	CAC His	ACG Thr	CAC His 35	TTC Phe 35	TCG Ser	GAG Glu	CTC Leu	CTA Leu 40	GAC Asp	GAG Glu	TTT Phe	TCC Ser	CAG Gln 45	AAC Asn	GTC Val	444
CTG Leu	GGT Gly 50	CAG Gln 50	CTC Leu	CTG Leu	AGT Ser	GAC Asp	CCT Pro 55	TTC Phe	CTC Leu	TCA Ser	GAG Glu	AAG Lys 60	AGC Ser	GAG Glu	TCA Ser	492
ATG Met 65	GAG Glu 65	GTG Val	GAG Glu	CCA Pro	TCT Ser	CCA Pro 70	ACA Thr	TCA Ser	CCA Pro	GCG Ala	CCT Pro 75	CTC Leu	ATC Ile	CAG Gln	GCT Ala	540
GAA Glu 80	CAC His	AGC Ser	TAC Tyr	TCT Ser	CTG Leu 85	AGC Ser	GAG Glu	GAG Glu	CCC Pro	CGG Arg 90	ACT Thr	CAG Gln	TCA Ser	CCA Pro	TTT Phe 95	588
ACC Thr	CAT His	GCG Ala	GCT Ala	ACC Thr 100	AGC Ser	GAC Asp	AGC Ser	TTC Phe	AAT Asn 105	GAC Asp	GAG Glu	GAG Glu	GTG Val	GAG Glu 110	AGT Ser	636
GAA Glu	AAA Lys	TGG Trp	TAC Tyr 115	CTG Leu	TCT Ser	ACA Thr	GAG Glu	TTT Phe 120	CCT Pro	TCA Ser	GCT Ala	ACC Thr	ATC Ile 125	AAG Lys	AAA Lys	684
GAG Glu	CCA Pro	ATC Ile 130	ACA Thr	GAG Glu	GAG Glu	CAG Gln	CCC Pro 135	CCG Pro	GGA Gly	CTT Leu	GTC Val	CCT Pro 140	TCT Ser	GTC Val	ACT Thr	732
CTG Leu 145	ACC Thr	ATC Ile	ACA Thr	GCC Ala	ATT Ile	TCC Ser	ACT Thr	CCT Pro	TTT Phe	GAA Glu	AAA Lys	GAA Glu	GAG Glu	TCC Ser	CCT Pro	780
CTG Leu 160	GAT Asp	ATG Met	AAT Asn	GCT Ala	GGG Gly 165	GGG Gly	GAC Asp	TCC Ser	TCA Ser	TGC Cys	CAG Gln	ACG Thr	CTT Leu	ATT Ile	CCT Pro 175	828
AAG Lys	ATT Ile	AAG Lys	CTG Leu	GAG Glu 180	CCC Pro	CAC His	GAA Glu	GTG Val	GAT Asp	CAG Gln	TTC Phe	TTA Leu	AAC Asn	TTC Phe 190	TCC Ser	876
CCG Pro	AAA Lys	GAA Glu	GCC Ala	TCC Ser	GTG Val	GAT Asp	CAA Gln	CTG Leu	CAC His	TTA Leu	CCA Pro	CCA Pro	ACA Thr	CCA Pro	CCC Pro	924
AGT Ser	AGT Ser	CAC His 210	AGC Ser	AGT Ser	GAC Asp	TCT Ser	GAG Glu	GGC Gly	AGC Ser	TTG Leu	AGC Ser	CCC Pro	AAC Asn	CCA Pro	CGC Arg	972
CTG Leu 225	CAT His	CCC Pro	TTC Phe	AGC Ser	CTG Leu	TCT Ser 230	CAG Gln	GCC Ala	CAC His	AGC Ser	CCT Pro 235	GTC Val	AGA Arg	GCC Ala	ATG Met	1020
CCC Pro 240	CGG Arg	GGC Gly	CCC Pro	TCT Ser	GCC Ala 245	TTG Leu	TCC Ser	ACA Thr	TCT Ser	CCT Pro 250	CTC Leu	CTC Leu	ACA Thr	GCT Ala	CCA Pro 255	1068
CAT His	AAG Lys	CTG Leu	CAG Gln	GGA Gly 260	TCG Ser	GGC Gly	CCC Pro	CTG Leu	GTC Val 265	CTG Leu	ACA Thr	GAA Glu	GAG Glu	GAG Glu	AAG Lys 270	1116

AGG ACC CTG GTT GCC GAG GGC TAT CCC ATT CCC ACC AAG CTG CCT CTG	1164
Arg Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu	
275 280 285	
ACA AAA TCT GAG GAG AAG GCC CTG AAG AAA ATC CGG AGA AAG ATC AAG	1212
Thr Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys	
290 295 300	
AAT AAG ATT TCT GCC CAA GAA AGC AGG AGA AAG AAG AAA GAA TAC ATG	1260
Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met	
305 310 315	
GAC AGC CTG GAG AAA AAA GTG GAG TCT TGT TCA ACT GAG AAC TTG GAG	1308
Asp Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu	
320 325 330 335	
CTT CGG AAG AAG GTG GAG GTG CTG GAG AAC ACC AAT AGG ACT CTC CTT	1356
Leu Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu	
340 345 350	
CAG CAA CTT CAG AAG CTT CAG ACT TTG GTG ATG GGG AAG GTC TCT CGA	1404
Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg	
355 360 365	
ACC TGC AAG TTA GCT GGC ACA CAG ACT GGC ACC TGC CTC ATG GTC GTT	1452
Thr Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val	
370 375 380	
GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG	1500
Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly	
385 390 395	
CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG	1548
Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu	
400 405 410 415	
TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC	1596
Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile	
420 425 430	
TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG TCG AGC CCA GCC TCA ACC	1644
Tyr Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr	
435 440 445	
GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG	1692
Gly Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser	
450 455 460	
TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC	1740
Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile	
465 470 475	
TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG	1788
Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln	
480 485 490 495	
CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA	1836
His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val	
500 505 510	
GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCCTCC	1886
Glu Leu Glu Arg Arg Val Asn Ala Thr Phe	
515 520	
TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTTCCCC TTCACCACTG GATCTCGAGG	1946
AGGAGATGGC TAGTGTTACG GCTCGAGACA GGAGGCCAGC CCAGGGGGTT CTGCTTATGT	2006

GTCCCCGTGG	CTCTCCACAA	AAGGGAGCTA	GCACCTCTCC	ATCCCTTTCT	CTTACTGCCA	2066
TTGGAAATTA	TTTTAGGGCT	GAGATAGGGG	TGGAACGAGC	AGGCTTGTTT	CCACCAATAG	2126
TGCCAAGAAG	ACACTGCCTG	ATTCTTCCCC	GGGAGGAGTG	ACTCCTCTGA	AGAAGACATG	2186
ACTCATGTTC	AGTTGAGACC	CCAGACTCTA	GCCACACACA	TGCCACAGAC	ATGCCAGGGA	2246
GTGGCAAAGC	ACTGACTCCT	GAGCTCCCTT	CCTCACTAGG	ACTCCAGTGT	GACCCTGCAC	2306
TGAGAGGACC	AAAGCGTCAT	TGCAGTCTTC	TCTCCACCCT	GTACCCCGGA	GTCCTGATTG	2366
GATGTCTGCA	GAGGCAGATG	GGGCTCCCAC	CATATTTTCA	GGCCGCAAGT	GCAATTCCTG	2426
AAGGCATCAG	GCTCTTCTCT	CCCAGGCTCT	CCTGCCCCCT	GTGTTGTTTG	TAGGACACCC	2486
CCACACCCAC	TCATACACAG	CCTGCATCTC	CACAGGACAA	TAGCTCTGTC	TCCCTGGCCT	2546
CCCCTCCCCA	TTTGTAATA	GTATTTATTA	GCTTGCTCAA	GCTCCCAGCT	GGCCATAGTG	2606
AAAAGATTTT	CCCTTTCAAC	CAGCAAAGTC	TTCTGTTGGC	CTTTGGAACA	GGAGAGTCCC	2666
CGGAATCTAG	GACCCTAGTC	TTTGTACTTG	ATGCCTTGTT	TCCCCCCTTT	TCTTCTTTAA	2726
AATTGGGGAC	CTATAACATC	ATCGCTGTTG	CGGAATCCAC	TTAGGCATGT	GTCCCCTGAT	2786
GGATGAATAC	ATGGGAATGG	TGGATACTGT	CTTCTGACTC	AGGCTCTAGG	CTCCATGGCT	2846
TCCTCTCTCT	GGTCCTGCCA	CACAGAAGGA	AAGCCCTGTC	CAGGATAATG	AGCGTTGCTG	2906
ACACCCTTGC	TAGCTTGTC	TGCCTACCTG	CTTACCCAC	TCCCTCACCT	TCCTCCTTCC	2966
CTTCTGCCCT	CCATCCACCT	GCCTTAACTA	ATTGGGGCTG	GAGTTGGTCA	TTTTTTGTAC	3026
ACCCACAGTG	GTACCTTTTA	CAGTCAGGTT	TGGATACTTT	GCAGCTCATC	CAAAGAGACA	3086
TAACTAAACC	CTAAACTCTT	TTTTTGTTGT	TGTTGTTGTT	GTTTTTTTTT	TTTATGATTA	3146
AAAAGTAAAA	ATTGTAGTTT	AAAAAAAAAA	AAAAAAACT	CGAG		3190

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg
 1          5          10          15
Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr
          20          25          30
His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
          35          40          45
Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met
          50          55          60
Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
          65          70          75          80
His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr
          85          90          95
His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu
          100          105          110
Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu
          115          120          125
Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu
          130          135          140
Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu
          145          150          155          160
Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys
          165          170          175
Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro
          180          185          190
Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser
          195          200          205
Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu
          210          215          220
His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro
          225          230          235          240
Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His
          245          250          255
Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg
          260          265          270
Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr
          275          280          285
Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn
          290          295          300

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Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp
 305 310 315 320
 Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu
 325 330 335
 Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln
 340 345 350
 Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr
 355 360 365
 Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val
 370 375 380
 Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro
 385 390 395 400
 Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser
 405 410 415
 Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr
 420 425 430
 Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly
 435 440 445
 Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser
 450 455 460
 Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser
 465 470 475 480
 Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His
 485 490 495
 Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu
 500 505 510
 Leu Glu Arg Arg Val Asn Ala Thr Phe
 515 520

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCT AATGGAGCTG AGAGTCGGG

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCG CTCATCGGTG CACGACAGA

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ACAGCTCCAC ATAAGCTGC

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAATTCGCT CAAGGAGAGT CCTATTGG

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: (26)...(129)
 - (C) OTHER INFORMATION: N = unknown or other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGTCAGTT CAGCGGATCC TGTCGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120

NNNNNNNNNG AGGCGAATTC AGTGCAACTG CAGC 154

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTCAGTT CAGCGGATCC TGTCG

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCAGTTG CACTGAATTC GCCTC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATCGGGCC GCCGAGATCT CATATGGAGC TGAGAGTC

38

A Cont